

RAW SEQUENCE LISTING
PATENT APPLICATION: US/08/485,943.1DATE: 12/06/96
TIME: 15:31:17

INPUT SET: S14270.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

(1) General Information:

- (i) APPLICANT: THE ROCKEFELLER UNIVERSITY
- (ii) TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING NUCLEIC ACIDS
- (iii) NUMBER OF SEQUENCES: 98
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: Klauber & Jackson
 - (B) STREET: 411 Hackensack Avenue
 - (C) CITY: Hackensack
 - (D) STATE: New Jersey
 - (E) COUNTRY: USA
 - (F) ZIP: 07601
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER: 08/485,943
 - (B) FILING DATE: June 7, 1995
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER: 08/438,431
 - (B) FILING DATE: May 10, 1995
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER: 08/347,563
 - (B) FILING DATE: November 30, 1994
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER: 08/292,345
 - (B) FILING DATE: August 17, 1994
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
- (A) NAME: Jackson Esq., David A.

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140
12-12-96

RAW SEQUENCE LISTING

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47 (B) REGISTRATION NUMBER: 26,742
 48 (C) REFERENCE/DOCKET NUMBER: 600-1-087 CIP2I
 49
 50 (ix) TELECOMMUNICATION INFORMATION:
 51 (A) TELEPHONE: 201 487-5800
 52 (B) TELEFAX: 201 343-1684
 53 (C) TELEX: 133521
 54
 55 (2) INFORMATION FOR SEQ ID NO:1:
 56
 57 (i) SEQUENCE CHARACTERISTICS:
 58 (A) LENGTH: 2793 base pairs
 59 (B) TYPE: nucleic acid
 60 (C) STRANDEDNESS: double
 61 (D) TOPOLOGY: linear
 62
 63 (ii) MOLECULE TYPE: DNA (genomic)
 64 (A) DESCRIPTION: Murine ob cDNA
 65
 66 (iii) HYPOTHETICAL: NO
 67
 68 (iv) ANTI-SENSE: NO
 69
 70 (vi) ORIGINAL SOURCE:
 71 (A) ORGANISM: Murine
 72
 73 (ix) FEATURE:
 74 (A) NAME/KEY: CDS
 75 (B) LOCATION: 57..560
 76
 77
 78 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
 79
 80 GGATCCCTGC TCCAGCAGCT GCAAGGTGCA AGAAGAAGAA GATCCCAGGG AGGAAA 56
 81
 82 ATG TGC TGG AGA CCC CTG TGT CGG TTC CTG TGG CTT TGG TCC TAT CTG 104
 83 Met Cys Trp Arg Pro Leu Cys Arg Phe Leu Trp Leu Trp Ser Tyr Leu
 84 1 5 10 15
 85
 86 TCT TAT GTT CAA GCA GTG CCT ATC CAG AAA GTC CAG GAT GAC ACC AAA 152
 87 Ser Tyr Val Gln Ala Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys
 88 20 25 30
 89
 90 ACC CTC ATC AAG ACC ATT GTC ACC AGG ATC AAT GAC ATT TCA CAC ACG 200
 91 Thr Leu Ile Lys Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr
 92 35 40 45
 93
 94 CAG TCG GTA TCC GCC AAG CAG AGG GTC ACT GGC TTG GAC TTC ATT CCT 248
 95 Gln Ser Val Ser Ala Lys Gln Arg Val Thr Gly Leu Asp Phe Ile Pro
 96 50 55 60
 97
 98 GGG CTT CAC CCC ATT CTG AGT TTG TCC AAG ATG GAC CAG ACT CTG GCA 296
 99 Gly Leu His Pro Ile Leu Ser Leu Ser Lys Met Asp Gln Thr Leu Ala

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	65	70	75	80	
100					
101					
102	GTC TAT CAA CAG	GTC CTC ACC AGC	CTG CCT TCC CAA AAT	GTG CTG CAG	344
103	Val Tyr Gln Gln	Val Leu Thr Ser	Leu Pro Ser Gln	Asn Val Leu Gln	
104		85	90	95	
105					
106	ATA GCC AAT GAC	CTG GAG AAT CTC	CGA GAC CTC CTC	CAT CTG CTG GCC	392
107	Ile Ala Asn Asp	Leu Glu Asn Leu	Arg Asp Leu Leu	His Leu Leu Ala	
108		100	105	110	
109					
110	TTC TCC AAG AGC	TGC TCC CTG CCT	CAG ACC AGT GGC	CTG CAG AAG CCA	440
111	Phe Ser Lys Ser	Cys Ser Leu Pro	Gln Thr Ser Gly	Leu Gln Lys Pro	
112		115	120	125	
113					
114	GAG AGC CTG GAT	GGC GTC CTG GAA	GCC TCA CTC TAC	TCC ACA GAG GTG	488
115	Glu Ser Leu Asp	Gly Val Leu Glu	Ala Ser Leu Tyr	Ser Thr Glu Val	
116		130	135	140	
117					
118	GTG GCT TTG AGC	AGG CTG CAG GGC	TCT CTG CAG GAC	ATT CTT CAA CAG	536
119	Val Ala Leu Ser	Arg Leu Gln Gly	Ser Leu Gln Asp	Ile Leu Gln Gln	
120	145	150	155	160	
121					
122	TTG GAT GTT AGC	CCT GAA TGC TGA	AGTTTCAAAG GCCACCAGGC	TCCCAAGA	588
123	Leu Asp Val Ser	Pro Glu Cys *			
124		165			
125					
126	ATCATGTAGA GGGAAGAAAC	CTTGGCTTCC AGGGGTCTTC	AGGAGAAGAG AGCCATGTGC		648
127					
128	ACACATCCAT CATTCAATTC	TCTCCCTCCT GTAGACCACC	CATCCAAAGG CATGACTCCA		708
129					
130	CAATGCTTGA CTCAAGTTAT	CCACACAACCT TCATGAGCAC	AAGGAGGGGC CAGCCTGCAG		768
131					
132	AGGGGACTCT CACCTAGTTC	TTGAGCAAGT AGAGATAAGA	GCCATCCCAT CCCCTCCATG		828
133					
134	TCCCACCTGC TCCGGGTACA	TGTTCTCTCCG TGGGTACACG	CTTCGCTGCG GCCCAGGAGA		888
135					
136	GGTGAGGTAG GGATGGGTAG	AGCCTTTGGG CTGTCTCAGA	GTCTTTGGGA GCACCGTGAA		948
137					
138	GGCTGCATCC ACACACAGCT	GGAAACTCCC AAGCAGCACA	CGATGGAAGC ACTTATTTAT		1008
139					
140	TTATTCTGCA TTCTATTTTG	GATGGATCTG AAGCAAGGCA	TCAGCTTTTT CAGGCTTTGG		1068
141					
142	GGGTCAGCCA GGATGAGGAA	GGCTCCTGGG GTGCTGCTTT	CAATCCTATT GATGGGTCTG		1128
143					
144	CCCGAGGCAA ACCTAATTTT	TGAGTGACTG GAAGGAAGGT	TGGGATCTTC CAAACAAGAG		1188
145					
146	TCTATGCAGG TAGCGCTCAA	GATTGACCTC TGGTGACTGG	TTTTGTTTCT ATTGTGACTG		1248
147					
148	ACTCTATCCA AACACGTTTG	CAGCGGCATT GCCGGGAGCA	TAGGCTAGGT TATTATCAAA		1308
149					
150	AGCAGATGAA TTTTGTCAAG	TGTAATATGT ATCTATGTGC	ACCTGAGGGT AGAGGATGTG		1368
151					
152	TTAGAGGGAG GGTGAAGGAT	CCGGAAGTGT TCTCTGAATT	ACATATGTGT GGTAGGCTTT		1428

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153							
154	TCTGAAAGGG	TGAGGCATTT	TCTTACCTCT	GTGGCCACAT	AGTGTGGCTT	TGTGAAAAGG	1488
155							
156	ACAAAGGAGT	TGACTCTTTC	CGGAACATTT	GGAGTGTACC	AGGCACCCTT	GGAGGGGCTA	1548
157							
158	AAGCTACAGG	CCTTTTGTTG	GCATATTGCT	GAGCTCAGGG	AGTGAGGGCC	CCACATTTGA	1608
159							
160	GACAGTGAGC	CCCAAGAAAA	GGGTCCCTGG	TGTAGATCTC	CAAGGTTGTC	CAGGGTTGAT	1668
161							
162	CTCACAATGC	GTTTCTTAAG	CAGGTAGACG	TTTGCATGCC	AATATGTGGT	TCTCATCTGA	1728
163							
164	TTGGTTCATC	CAAAGTAGAA	CCCTGTCTCC	CACCCATTCT	GTGGGGAGTT	TTGTTCCAGT	1788
165							
166	GGGAATGAGA	AATCACTTAG	CAGATGGTCC	TGAGCCCTGG	GCCAGCACTG	CTGAGGAAGT	1848
167							
168	GCCAGGGCCC	CAGGCCAGGC	TGCCAGAATT	GCCCTTCGGG	CTGGAGGATG	AACAAAGGGG	1908
169							
170	CTTGGGTTTT	TCCATCACCC	CTGCACCCTA	TGTCACCATC	AAACTGGGGG	GCAGATCAGT	1968
171							
172	GAGAGGACAC	TTGATGGAAA	GCAATACACT	TTAAGACTGA	GCACAGTTTC	GTGCTCAGCT	2028
173							
174	CTGTCTGGTG	CTGTGAGCTA	GAGAAGCTCA	CCACATACAT	ATAAAAATCA	GAGGCTCATG	2088
175							
176	TCCCTGTGGT	TAGACCCTAC	TCGCGGCGGT	GTACTCCACC	ACAGCAGCAC	CGCACCGCTG	2148
177							
178	GAAGTACAGT	GCTGTCTTCA	ACAGGTGTGA	AAGAACCTGA	GCTGAGGGTG	ACAGTGCCCA	2208
179							
180	GGGGAACCCT	GCTTGCAGTC	TATTGCATTT	ACATACCGCA	TTTCAGGGCA	CATTAGCATC	2268
181							
182	CACTCCTATG	GTAGCACACT	GTTGACAATA	GGACAAGGGA	TAGGGGTTGA	CTATCCCTTA	2328
183							
184	TCCAAAATGC	TTGGGACTAG	AAGAGTTTTG	GATTTTAGAG	TCTTTTCAGG	CATAGGTATA	2388
185							
186	TTTGAGTATA	TATAAAATGA	GATATCTTGG	GGATGGGGCC	CAAGTATAAA	CATGAAGTTC	2448
187							
188	ATTTATATTT	CATAATACCG	TATAGACACT	GCTTGAAGTG	TAGTTTTATA	CAGTGTTTTA	2508
189							
190	AATAACGTTG	TATGCATGAA	AGACGTTTTT	ACAGCATGAA	CCTGTCTACT	CATGCCAGCA	2568
191							
192	CTCAAAAACC	TTGGGGTTTT	GGAGCAGTTT	GGATCTTGGG	TTTTCTGTTA	AGAGATGGTT	2628
193							
194	AGCTTATACC	TAAAACCATA	ATGGCAAACA	GGCTGCAGGA	CCAGACTGGA	TCCTCAGCCC	2688
195							
196	TGAAGTGTGC	CCTTCCAGCC	AGGTCATACC	CTGTGGAGGT	GAGCGGGATC	AGGTTTTGTG	2748
197							
198	GTGCTAAGAG	AGGAGTTGGA	GGTAGATTTT	GGAGGATCTG	AGGGC		2793

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 167 amino acids

(B) TYPE: amino acid

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PATENT APPLICATION US/08/485,943A

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206 (D) TOPOLOGY: linear

207

208 (ii) MOLECULE TYPE: protein

209 (A) DESCRIPTION: Murine ob polypeptide

210

211 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

212

213 Met Cys Trp Arg Pro Leu Cys Arg Phe Leu Trp Leu Trp Ser Tyr Leu

214 1 5 10 15

215

216 Ser Tyr Val Gln Ala Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys

217 20 25 30

218

219 Thr Leu Ile Lys Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr

220 35 40 45

221

222 Gln Ser Val Ser Ala Lys Gln Arg Val Thr Gly Leu Asp Phe Ile Pro

223 50 55 60

224

225 Gly Leu His Pro Ile Leu Ser Leu Ser Lys Met Asp Gln Thr Leu Ala

226 65 70 75 80

227

228 Val Tyr Gln Gln Val Leu Thr Ser Leu Pro Ser Gln Asn Val Leu Gln

229 85 90 95

230

231 Ile Ala Asn Asp Leu Glu Asn Leu Arg Asp Leu Leu His Leu Leu Ala

232 100 105 110

233

234 Phe Ser Lys Ser Cys Ser Leu Pro Gln Thr Ser Gly Leu Gln Lys Pro

235 115 120 125

236

237 Glu Ser Leu Asp Gly Val Leu Glu Ala Ser Leu Tyr Ser Thr Glu Val

238 130 135 140

239

240 Val Ala Leu Ser Arg Leu Gln Gly Ser Leu Gln Asp Ile Leu Gln Gln

241 145 150 155 160

242

243 Leu Asp Val Ser Pro Glu Cys

244 165

245

246

247 (2) INFORMATION FOR SEQ ID NO:3:

248

249 (i) SEQUENCE CHARACTERISTICS:

250 (A) LENGTH: 700 base pairs

251 (B) TYPE: nucleic acid

252 (C) STRANDEDNESS: double

253 (D) TOPOLOGY: linear

254

255 (ii) MOLECULE TYPE: cDNA

256 (A) DESCRIPTION: Human ob cDNA where N represents any nucleotide

257

258 (iii) HYPOTHETICAL: NO